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<170> PatentIn version 3.1

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ttg cct gat ctc gat acc acc aag gat gtg gtc aag aat gaa tgg tac				624
Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr				
	195	200	205	
gac tgg gtg gga tca ttg gta tgc aac tac tcc att gac ggc ctc cgt				672
Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg				
	210	215	220	
atc gac aca gta aaa cac gtc cag aag gac ttc tgg ccc ggg tac aac				720
Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn				
	225	230	235	240
aaa gcc gca ggc gtg tac tgt atc ggc gag gtg ctc gac ggt gat ccg				768
Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro				
	245	250	255	
gcc tac act tgt ccc tac cag aac gtc atg gac ggc gta ctg aac tat				816
Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr				
	260	265	270	
ccc att tac tat cca ctc ctc aac gcc ttc aag tca acc tcc ggc agc				864
Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser				
	275	280	285	
atg gac gac ctc tac aac atg atc aac acc gtc aaa tcc gac tgt cca				912
Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro				
	290	295	300	
gac tca aca ctc ctg ggc aca ttc gtc gag aac cac gac aac cca cgg				960
Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg				
	305	310	315	320
ttc gct tct tac acc aac gac ata gcc ctc gcc aag aac gtc gca gca				1008
Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala				
	325	330	335	
ttc atc atc ctc aac gac gga atc ccc atc atc tac gcc ggc caa gaa				1056
Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu				
	340	345	350	
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Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp				
	355	360	365	
ctc tgc ggc tac ccg acc gac agc gag ctg tac aag tta att gcc tcc				1152
Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser				
	370	375	380	
gcg aac gca atc ccg aac tat gcc att agc aaa gat aca gga ttc gtg				1200
Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val				
	385	390	395	400
acc tac aag aac tgg ccc atc tac aaa gac gac aca acg atc gcc atg				1248
Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met				

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ggg gct tcg ggt gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac      1344
Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
              435              440              445
aca gcc ggc cag caa ttg acg gag gtc att ggc tgc acg acc gtg acg      1392
Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
              450              455              460
gtt ggt tcg gat gga aat gtg cct gtt cct atg gca ggt ggg cta cct      1440
Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
              465              470              475              480
agg gta ttg tat ccg act gag aag ttg gca ggt agc aag atc tgt agt      1488
Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
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agc tcg tga
Ser Ser

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<210> 11

<211> 498

<212> PRT

<213> *Aspergillus niger*

<400> 11

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Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
              35              40              45
Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
              50              55              60
Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
65              70              75              80
Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
              85              90              95
Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
              100              105              110
Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
              115              120              125
Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
              130              135              140
Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
145              150              155              160
Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
              165              170              175
Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
              180              185              190
Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
              195              200              205
Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
              210              215              220
Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
225              230              235              240

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Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
 245 250 255
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 260 265 270
 Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
 275 280 285
 Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
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 Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
 305 310 315 320
 Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
 325 330 335
 Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
 340 345 350
 Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
 355 360 365
 Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
 370 375 380
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 Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
 420 425 430
 Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
 435 440 445
 Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
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 Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
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<210> 12

<211> 3697

<212> DNA

<213> *Aspergillus niger*

<400> 12

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agtacc	a	tac	agtacc	gcgt	tatgaaaa	ca	cattaat	ccg	gaccc	240
tagcgt	g	ctt	ggcattag	gg	ttcgaaaa	ac	aatcga	agag	tataag	300
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aaaacgc	c	tt	atacaatt	aa	gcagtt	aa	ag	ttaga	at	420
aaaaat	c	gat	ctcgcag	tcc	cgattc	gcct	atcaaaa	acca	gttta	480
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gccata	c	agg	cagatag	acc	tctacct	att	aaatcgg	c	ctaggc	720
tgttct	g	gct	gtgggt	taca	ggggcata	aaa	attacgc	act	accgaa	780
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<211> 1497

<212> DNA

<213> *Aspergillus niger*

<220>

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 Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr
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 ttc ctt ctc acg gat cga ttt gca agg acg gat ggg tcg acg act gcg 144
 Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
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 Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
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 Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
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 aac tac ggc act gca gat gac ttg aag gcg ctc tct tcg gcc ctt cat 384
 Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
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 atc gac aca gta aaa cac gtc cag aag gac ttc tgg ccc ggg tac aac 720
 Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
 225 230 235 240
 aaa gcc gca ggc gtg tac tgt atc ggc gag gtg ctc gac ggt gat ccg 768
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Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
305      310      315      320
ttc gct tct tac acc aac gac ata gcc ctc gcc aag aac gtc gca gca      1008
Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
      325      330      335
ttc atc atc ctc aac gac gga atc ccc atc atc tac gcc ggc caa gaa      1056
Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
      340      345      350
cag cac tac gcc ggc gga aac gac ccc gcg aac cgc gaa gca acc tgg      1104
Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
      355      360      365
ctc tcg ggc tac ccg acc gac agc gag ctg tac aag tta att gcc tcc      1152
Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
      370      375      380
gcg aac gca atc cgg aac tat gcc att agc aaa gat aca gga ttc gtg      1200
Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
      385      390      395      400
acc tac aag aac tgg ccc atc tac aaa gac gac aca acg atc gcc atg      1248
Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
      405      410      415
cgc aag ggc aca gat ggg tcg cag atc gtg act atc ttg tcc aac aag      1296
Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
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Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
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aca gcc ggc cag caa ttg acg gag gtc att ggc tgc acg acc gtg acg      1392
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Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
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Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
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agc tcg tga
Ser Ser

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<210> 14

<211> 498

<212> PRT

<213> Aspergillus niger

<400> 14

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Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
      35      40      45
Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
      50      55      60
Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile

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Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
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Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
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Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
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Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
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Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
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<211> 3570

<212> DNA

<213> *Aspergillus niger*

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Tyr Phe Leu Leu Thr Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr
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His Ala Arg Gly Met Tyr Leu Met Val Asp Val Val Pro Asn His Met
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Gly Tyr Ala Gly Asn Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro
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ttc gat tcc tcc tcc tac ttc cac cca tac tgc ctg atc aca gat tgg 528
Phe Asp Ser Ser Ser Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp
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Pro	Arg	Val	Leu	Leu	Pro	Ala	Ser	Val	Val	Asp	Ser	Ser	Ser	Leu	Cys	
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Arg Ile Asp Ser Val Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr
225 230 235 240
Gln Glu Ala Ala Gly Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn
245 250 255
Pro Ala Leu Asp Cys Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn
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<212> DNA

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<210> 19

<211> 1977

<212> DNA

<213> *Penicillium chrysogenum*

<220>

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<400> 19

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Asn Glu Asp Asp Arg Gly Asp Leu Ser Tyr Pro His Cys Tyr Leu Tyr
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Thr Asp Leu Asp Val Pro Ser Ala Gln Glu Val Lys Gln Leu Arg Ser
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405	410	430	450	470	490	510	530	550	570	590	610	630	650	670	690	710			
410	415	435	455	475	495	515	535	555	575	595	615	635	655	675	695	715			
415	420	440	460	480	500	520	540	560	580	600	620	640	660	680	700	720			
420	425	445	465	485	505	525	545	565	585	605	625	645	665	685	705	725			
425	430	450	470	490	510	530	550	570	590	610	630	650	670	690	710	730			
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465	470	490	510	530	550	570	590	610	630	650	670	690	710	730	750	770			
470	475	495	515	535	555	575	595	615	635	655	675	695	715	735	755	775			
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atc atc atc cct cag cgt gca aat gac tat gcg tct ctt gcg ttg tct			1152
Ile Ile Ile Pro Gln Arg Ala Asn Asp Tyr Ala Ser Leu Ala Leu Ser			
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tct ctc att cat gca ctc tac gaa ttg gag tcc tat gcg gtt gcc cgc			1200
Ser Leu Ile His Ala Leu Tyr Glu Leu Glu Ser Tyr Ala Val Ala Arg			
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Leu Val Thr Lys Glu Ser Lys Pro Pro Met Leu Val Leu Leu Ala Pro			
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Ser Ile Glu Ala Asp Tyr Glu Cys Leu Ile Glu Val Gln Leu Pro Phe			
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act gtc tct ggc aag gtg gtg act gaa cat cga aac ctc cca agc gtg			1392
Thr Val Ser Gly Lys Val Thr Glu His Arg Asn Leu Pro Ser Val			
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Ala Leu Lys Asp Ala Met Ser Asn Tyr Val Asp Ser Met Asp Phe Val			
465	470	475	480
acc aca aac gac gaa ggg caa gcc act gac gat ctc cca atc gac gag			1488
Thr Thr Asn Asp Glu Gly Gln Ala Thr Asp Asp Leu Pro Ile Asp Glu			
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Ser Phe Ser Pro Leu Leu His Arg Ile Glu Ser Ala Val Arg Tyr Arg			
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Ala Val His Pro Asn Asp Pro Val Leu Asp Pro Ser Glu Arg Leu Thr			
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gaa ttc gca cac ccc tca gaa gac atg gtc aag aac tcc aaa tcc cat			1632
Glu Phe Ala His Pro Ser Glu Asp Met Val Lys Asn Ser Lys Ser His			
530	535	540	
ctt gag aaa ttg atg tcc ata gca gat gtc aag aaa gtt cca ccg aag			1680
Leu Glu Lys Leu Met Ser Ile Ala Asp Val Lys Lys Val Pro Pro Lys			
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aca aaa ggc cgt aaa cgc caa cgt gaa aca gag aaa cct ctc tca ggt			1728
Thr Lys Gly Arg Lys Arg Gln Arg Glu Thr Glu Lys Pro Leu Ser Gly			
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Leu Asp Val Asp Ala Leu Leu Ser Leu Glu Pro Lys Arg Thr Lys Ile			
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Ser Thr Glu Asn Ala Ile Pro Glu Phe Lys Gln Thr Leu Ser Arg Ala			
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gaa aac atc gac gca atc cac gac gct gtg cag cag atg gct aaa atc			1872
Glu Asn Ile Asp Ala Ile His Asp Ala Val Gln Gln Met Ala Lys Ile			
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Ile Glu Ser Gln Ile Thr His Ser Leu Gly His Ser Asn Tyr Asp Arg			
625	630	635	640
gtt atc gag ggg ctt ggt act atg cgt gaa gaa ctg gtg gac tat gag			1968
Val Ile Glu Gly Leu Gly Thr Met Arg Glu Glu Leu Val Asp Tyr Glu			
645	650	655	
gaa ccg gcg gtg tac aat gac ttt gtg cgt cag ttg aag ggc aag atg			2016
Glu Pro Ala Val Tyr Asn Asp Phe Val Arg Gln Leu Lys Gly Lys Met			

660	665	670	
ttg cgg gag gag ctg ggt ggg gat	cgg agg gag ctg	tggtgg ttt gta	2064
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Arg Lys Gly Lys Leu Gly Leu Ile	Gly Lys Ser Glu Val Asp Ser Ser		
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gct gtt gag gag caa gag gct caa	gag ttt ctg gct ccc aat tga	2157	
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<211> 718

<212> PRT

<213> Penicillium chrysogenum

<400> 23

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20 25 30	
Met Gln Tyr Val Trp Asp Arg Ile Thr Ala Thr Val Ala Thr Gly Arg	
35 40 45	
Lys Thr Ala Thr Val Gly Val Val Gly Leu Arg Thr Asp Val Ser Thr	
50 55 60	
His Trp Asp Pro Cys Leu Met Phe Gly Thr Gly Thr Ile Asn Asp Leu	
65 70 75 80	
Glu Glu Glu Ser Phe Ser Asn Ile Ser Ile Leu Phe Gly Leu Gly Gln	
85 90 95	
Val Leu Met Pro Asp Ile Arg Lys Leu Arg Glu Thr Ile Lys Pro Ser	
100 105 110	
Asn Thr Asn Arg Gly Asp Ala Ile Ser Ser Ile Val Ile Ala Met Gln	
115 120 125	
Met Ile Ile Asp Tyr Thr Lys Lys Asn Lys Tyr Lys Arg Lys Ile Ile	
130 135 140	
Leu Val Thr Asn Gly Thr Gly Val Met Ser Asp Asp Asn Ile Glu Gly	
145 150 155 160	
Ile Ile Glu Lys Met Lys Glu Val Asn Ile Glu Leu Val Val Met Tyr	
165 170 175	
Tyr Gly Val Lys Glu Glu Asp Lys Asp Ser Arg Lys Ala Glu Asn Glu	
180 185 190	
Thr Phe Leu Arg Ser Leu Ala Glu Asp Cys Glu Gly Ala Tyr Gly Thr	
195 200 205	
Leu Glu Gln Ala Val Ser Glu Leu Asp Ile Pro Arg Ile Lys Val Thr	
210 215 220	
Lys Ser Met Pro Ser Phe Lys Gly Asn Leu Thr Leu Gly Asn Pro Glu	
225 230 235 240	
Glu Tyr Asp Thr Ala Met Thr Ile Pro Val Glu Arg Tyr Phe Arg Thr	
245 250 255	
Tyr Val Ala Lys Pro Ile Ser Ala Ser Ser Phe Val Pro Arg Ser Gly	
260 265 270	
Thr Glu Pro Gly Ser Gln Ala Pro Val Lys Gly Asp Ala Glu Gly Asp	
275 280 285	
Ala Leu Ala Ser Val Arg Thr Ser Arg Thr Tyr Gln Ile Thr Asp Glu	
290 295 300	
Ser Ala Pro Gly Gly Lys Ile Asp Val Glu Arg Asp Asp Leu Ala Lys	

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305          310          315          320
Gly Tyr Glu Tyr Gly Arg Thr Ala Val Pro Ile Glu Gln Thr Asp Glu
          325          330          335
Asn Val Ala Asn Leu Gln Thr Phe Ala Gly Met Gly Leu Ile Gly Phe
          340          345          350
Val Gln Lys Asp Gln Tyr Asp Arg Tyr Met His Met Ser Asn Thr Asn
          355          360          365
Ile Ile Ile Pro Gln Arg Ala Asn Asp Tyr Ala Ser Leu Ala Leu Ser
          370          375          380
Ser Leu Ile His Ala Leu Tyr Glu Leu Glu Ser Tyr Ala Val Ala Arg
385          390          395          400
Leu Val Thr Lys Glu Ser Lys Pro Pro Met Leu Val Leu Leu Ala Pro
          405          410          415
Ser Ile Glu Ala Asp Tyr Glu Cys Leu Ile Glu Val Gln Leu Pro Phe
          420          425          430
Ala Glu Asp Val Arg Ser Tyr Arg Phe Pro Pro Leu Asp Lys Ile Ile
          435          440          445
Thr Val Ser Gly Lys Val Val Thr Glu His Arg Asn Leu Pro Ser Val
          450          455          460
Ala Leu Lys Asp Ala Met Ser Asn Tyr Val Asp Ser Met Asp Phe Val
465          470          475          480
Thr Thr Asn Asp Glu Gly Gln Ala Thr Asp Asp Leu Pro Ile Asp Glu
          485          490          495
Ser Phe Ser Pro Leu Leu His Arg Ile Glu Ser Ala Val Arg Tyr Arg
          500          505          510
Ala Val His Pro Asn Asp Pro Val Leu Asp Pro Ser Glu Arg Leu Thr
          515          520          525
Glu Phe Ala His Pro Ser Glu Asp Met Val Lys Asn Ser Lys Ser His
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Leu Glu Lys Leu Met Ser Ile Ala Asp Val Lys Lys Val Pro Pro Lys
545          550          555          560
Thr Lys Gly Arg Lys Arg Gln Arg Glu Thr Glu Lys Pro Leu Ser Gly
          565          570          575
Leu Asp Val Asp Ala Leu Leu Ser Leu Glu Pro Lys Arg Thr Lys Ile
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Ser Thr Glu Asn Ala Ile Pro Glu Phe Lys Gln Thr Leu Ser Arg Ala
          595          600          605
Glu Asn Ile Asp Ala Ile His Asp Ala Val Gln Gln Met Ala Lys Ile
          610          615          620
Ile Glu Ser Gln Ile Thr His Ser Leu Gly His Ser Asn Tyr Asp Arg
625          630          635          640
Val Ile Glu Gly Leu Gly Thr Met Arg Glu Glu Leu Val Asp Tyr Glu
          645          650          655
Glu Pro Ala Val Tyr Asn Asp Phe Val Arg Gln Leu Lys Gly Lys Met
          660          665          670
Leu Arg Glu Glu Leu Gly Gly Asp Arg Arg Glu Leu Trp Trp Phe Val
          675          680          685
Arg Lys Gly Lys Leu Gly Leu Ile Gly Lys Ser Glu Val Asp Ser Ser
          690          695          700
Ala Val Glu Glu Gln Glu Ala Gln Glu Phe Leu Ala Pro Asn
705          710          715

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